

Fig. 1 (A)

CAGTGGCAGCAGGCAGTGGCAGCAGGCAGTGGCCCA	36
GGCAGAAATAGCTCCCGCGATTCACTGGAGCCTT	72
CCCCGGGCCCTGGTCCCAGCTACCGGGACTCGCGCG	108
TCCGGATCTCAAAAGCGGCAGAGGCCACCGAAGGGA	144
CAGGAAGCACTTTGGTCCAGACCACACTCCGGCAC	180
AGTGCAGAAAGAGCCGGCGGGAGCCACTCTGATCCC	216
GGACGCCTCAGCGCCCCCTGGGCTTGGCTTGCCT	252
TCGGGCCGGGAAGGCTGACCGCGATGCCAGGACGC	288
MetProGlyArg	4
GCTCCCCTCCGCACCGTCCCAGGCCTGGGTGCC	324
AlaProLeuArgThrValProGlyAlaLeuGlyAla	16
TGGCTGCTGGCGGCCTCTGGGCCTGGACCCTGTGC	360
TrpLeuLeuGlyGlyLeuTrpAlaTrpThrLeuCys	28
GGCCTGTGCAGCCTGGGGCGGTGGAGGCCCGCGC	396
GlyLeuCysSerLeuGlyAlaValGlyAlaProArg	40
CCGTGCCAGGCCGCAGCAGTGGGAGGGCGCCAG	432
ProCysGlnAlaProGlnGlnTrpGluGlyArgGln	52
GTTATGTACCAGCAAAGTAGCGGGCGAACAGCCGC	468
ValMetTyrGlnGlnSerSerGlyArgAsnSerArg	64
GCCCTGCTCTCCTACGACGGGCTAACCAAGCGCGTG	504
AlaLeuLeuSerTyrAspGlyLeuAsnGlnArgVal	76
CGGGTGCTGGACGAGAGGAAGGCGCTGATCCCCTGC	540
ArgValLeuAspGluArgLysAlaLeuIleProCys	88
AAGAGATTATTGAATATATTGCTGTATAAGGAT	576
LysArgLeuPheGluTyrIleLeuLeuTyrLysAsp	100

Fig. 1 (B)

GGAGTGATGTTCAGATTGACCAAGCCACCAAGCAG	612
GlyValMetPheGlnIleAspGlnAlaThrLysGln	112
TGCTCAAAGATGACCCTGACACAGCCCTGGGATCCT	648
CysSerLysMetThrLeuThrGlnProTrpAspPro	124
CTTGACATTCCCTCAAAACTCCACCTTGAAGACCAG	684
LeuAspIleProGlnAsnSerThrPheGluAspGln	136
TACTCCATCGGGGGGCCTCAGGAGCAGATCACCGTC	720
TyrSerIleGlyGlyProGlnGluGlnIleThrVal	148
CAGGAGTGGTCGGACAGAAAGTCAGCTAGATCCTAT	756
GlnGluTrpSerAspArgLysSerAlaArgSerTyr	160
GAAACCTGGATTGGCATCTATACTACAGTCAAGGATTGC	792
GlutThrTrpIleGlyIleTyrThrValLysAspCys	172
TATCCTGTCCAGGAAACCTTACCATAAACTACAGT	828
TyrProValGlnGluThrPheThrIleAsnTyrSer	184
GTGATATTGTCTACGCGGTTTTGACATCCAGCTG	864
ValIleLeuSerThrArgPhePheAspIleGlnLeu	196
GGTATTAAAGACCCCTCGGTGTTACCCCTCCAAGC	900
GlyIleLysAspProSerValPheThrProProSer	208
ACGTGCCAGATGGCCCAACTGGAGAAGATGAGCGAA	936
ThrCysGlnMetAlaGlnLeuGluLysMetSerGlu	220
GAUTGCTCCTGGTGAGCCTGTGCATAGGAAAGCGGC	972
AspCysSerTrp***	224
AGCATCGGATGTCAGCCCCCTGCGGCCAGCTGGA	1008
GATGGATATGAGACTAGTCAAGATGTGAATGCTAAT	1044
TGGAGAGAAATATAATTAGGAAGATGCACATTGA	1080

Fig. 1 (C)

TGTGGGGTTTGATGTCGATTGACTACTCAA	1116
GCTCTGTTACAGAAGAAAATTGAATGGCGAGGGTG	1152
TGCCCATATGAACGTGACTAGATGGCTAATATGGACA	1188
CTTGGGTATTCTAACGCTGTTCAAGGGCTGGTTT	1224
TCTGCATGCACGGTATAACACATAATGCAGTGCAT	1260
GCACATAGGAAAGGGTCAAGTAAGAGAAGTTGCCTT	1296
GGCAGCAAGTATTGTTGACATTATTAGAATT	1332
AGTGATAATAAAAGCAGAGTGATTTGGTCAATT	1368
TATTATTAATTCTAAATTCCCTGCAGAGAATGCC	1404
CCTTATTGCTGCACCAGGGTGGCATTGCTCCCAC	1440
TGAGCCCTACTCCACCCCTGTCCTGCACCCCTGG	1476
TTGCCAAAAAAATGATAACTTAAATCCCTCCAGAC	1512
TTAAGAATTATGGCATGGCCAATTGATATAAC	1548
ATTTAGAAGGAAATGAAAAGCTAAAATAGGAAGTAA	1584
TTATTCCCTCTAAAGAACATTGAGCAAGGCAGTT	1620
TAGAGAACCTAATGTCTACACTGGCATAGCACGAG	1656
CCATGTAAGCTCTTTTCTATGCAAGAGTATT	1692
GATGTATGTGCTGAATCTCACAGACTTGTCAATAC	1728
ACAGGCAGTATTCTAAAATAGCACTGAACAGGGAGT	1764
CAGGAGACTATTGTCTCCTAAACCCAGGACTAGAGT	1800
TCCCTCGTACTGTCACTCCTTGGTCATTAAATGCA	1836
CTGGGCTTGCCTGCACCTTGGCCTTCCTAGAACGCT	1872
GCTTCATAACCTCTGTCTGACTTCTGCATCTCCT	1908
TCCAGGTCAGCTCATTACAAGAGTTGCTCCCAAGC	1944
CTGGATGAGTTGCACCTTGCATCTGAGCATGCATT	1980
TCTCACAAATAATTATTAAGCTGTGATAATTCTG	2016
CTTTCAGGACACTCATCCATTATCTTGGCTGTGAGC	2052
TCCTTGGGTACGGTACCTTGTATGTTAATTAT	2088
ATCCCTAGCACAAAGCAAGTGCCTGGCACATAGTCA	2124
GTGCCCTAAGTATTGCTAGAGTGAAGAATGCCAGCC	2160
TCTCTTGTCCCTGGTTCTATGTGTTGAATGTGG	2196
TTGAGTTGTCCATTGCTAGGGAGAGACTTCCAGTA	2232
ATAAAATTACTATTCTAGATGCTTACTGTTATG	2268

Fig. 1 (D)

TTTTATCTGCCCATTTATCTTCTAGTTACCAAGGA	2304
GAAATGTGTGACACCTATATTATAATGAAAACAATC	2340
TTATTACTTATAGTTATCTATATTAAACAAATTAA	2376
ATTGCATTTAAAGCATTCTTGATATTGTTGCTTT	2412
TGCAATAAAATATGGATAATCTTGGTTATAAGGGAGT	2448
TAAAACAATGCTGTAATAAATAAAGTGTTCATGTG	2484
ATCAAAAAAAAAAAAAAA	2507

Fig. 2 (A)

CCAGACTCGGACCCCCAAGCCGGAAGCCTCTAAAAC	36
AGAAAATTGGAAAATCGGAAAATCAGGAGAGGCCAG	72
GGCTCCTGAGCTGGTCCCAGAGCACATCTTCCACCA	108
GCGCTCAGACAACGCGCGTGAECTCTCCCACGCCGGG	144
CCTCGGCTCCCTCCCAGGTTGGCTGACCCGGAGGG	180
CCGCGAATCACGATGCTCACACGCGCTCCCCGCCGC MetLeuThrArgAlaProArgArg	216 8
CTGGTCCAGGGGCCCGGGAGACCTGGCTGCTTGGC LeuValGlnGlyProArgGluThrTrpLeuLeuGly	252 20
GCCCTCTGGGTCTGGATATTGTGCGGCCTGGGGATG GlyLeuTrpValTrpIleLeuCysGlyLeuGlyMet	288 32
GCGGGCTCCCCGGGAACCCCGCAGCCATGCCAGGCG AlaGlySerProGlyThrProGlnProCysGlnAla	324 44
CCCCAGCAGTGGGAGGGACGTCAGGTTCTGTACCAG ProGlnGlnTrpGluGlyArgGlnValLeuTyrGln	360 56
CAGAGCAGCGGGCACAAACAGCCGCGCCCTGGTGTCC GlnSerSerGlyHisAsnSerArgAlaLeuValSer	396 68
TACGATGGTCTCAACCAGCGCGTGCAGGGTGCTGGAC TyrAspGlyLeuAsnGlnArgValArgValLeuAsp	432 80
GAAAGGAAGGCGCTGATCCCCTGCAAGAGATTATT GluArgLysAlaLeuIleProCysLysArgLeuPhe	468 92
GAATACATTTACTCTATAAGGATGGAGTGATGTTT GluTyrIleLeuLeuTyrLysAspGlyValMetPhe	504 104
CAGATTGAACAAGCCACCAAACGTGTGCAAAGATA GlnIleGluGlnAlaThrLysLeuCysAlaLysIle	540 116

Fig. 2 (B)

CCCTTGGCAGAACCTGGGATCCTCTCGACATTCCC ProLeuAlaGluProTrpAspProLeuAspIlePro	576 128
CAGAATTCTACCTTGAAAGATCAGTACTCTATCGGA GlnAsnSerThrPheGluAspGlnTyrSerIleGly	612 140
GGGCCTCAGGAGCAGATCATGGTCCAGGAATGGTCT GlyProGlnGluGlnIleMetValGlnGluTrpSer	648 152
GACAGGAGGACAGCCAGATCCTATGAAACCTGGATT AspArgArgThrAlaArgSerTyrGluThrTrpIle	684 164
GGCGTTATACAGCCAAGGATTGCTACCCGGTCCAG GlyValTyrThrAlaLysAspCysTyrProValGln	720 176
GAGACCTTCATTAGGAACTACACTGTGGCCTGTCC GluThrPheIleArgAsnTyrThrValValLeuSer	756 188
ACTCGGTTCTTGATGTGCAGTTGGCATTAAAGAC ThrArgPhePheAspValGlnLeuGlyIleLysAsp	792 200
CCCTCTGTGTTCACCCCCACCAAGCACGTGCCAGACA ProSerValPheThrProProSerThrCysGlnThr	828 212
GCACAGCCAGAGAAGATGAAAGAGAACTGCTCCCTG AlaGlnProGluLysMetLysGluAsnCysSerLeu	864 224
TGAATTCATGAGCGGAAGCCACGACCTCAGCTCT ***	900 224
TAGGGACTTGTGGAAATGGACTAGAGGCCAGTT GGAAAGCAACTCGTCACGAGAAGCAAAGCTAGTTTT	936 972
AGGAAGATAAACCTATGTGGACTTGCTTGTCACT GACTGTGGCTGCTCAGCTCTATTGGAAAGGAACC	1008 1044
TGGGTTATCCTTCTGTGTGCAGGTGTAGTCAGT GCTGTAGGGTAGGACGGGTGAAGGTGGGGCGCA	1080 1116

Fig. 2 (C)

CAAGGAGTTGCCTCTGCAGAGTGAACCTTTATTA	1152
TTGCCAATAAGATTGAAAGTGATAATAAGATATAGT	1188
ATAATTTTTTCAGTCTCTCCTTACAAAGAAAGTC	1224
CCTGCTTGTGCACTAGGGTAGTGACAGTTCCA	1260
CTGACCCCACACCTGCCTCTGGCTACTATGAGATGA	1296
CCCTTAAGATTCTTCCAAGCTAAATTTGTCAC	1332
ATGGCCCACC GGATGTAGATATTCTGCAAGGAAGTA	1368
GAAACTTGTAAATGCAAAGCAATGTTGCCTCTGAAGG	1404
GAAAAGAAGTTTAAGCGGGAGGCTTAGACAATCTT	1440
AGTATCTCATGTGAGATGAAGTCCGAGCCGTGT	1476
GGTGCTTGTGCAAGAGTACTGACTGCTGTGCTG	1512
AAACTATGTCTTTCTAGCGGGCAAACAGGCTTGCA	1548
AAACAGCACTGAATTGGGAGGCCCAAGTAAGGCC	1584
TAGGATTCTCTGCTACTCTAACCTTAAGTAGTAA	1620
ATGCACTAGGCTAACAGCTCTCGCCTGCCTTCTG	1656
GAAACTCTCTGTCTATATGACTACTGCTCACGCTTC	1692
CAACATCAGCTCACATGTGCCCTGTGAGCTGCTC	1728
CAATGCCTGAATTCAATTGCACCTTACAGCTTGGCAT	1764
GCCTTGCTCACAAACTCAGTATGCTGCGTGAGGAT	1800
TTCCTGATTACTGGAAACTAACCTCTGTTATCCTGG	1836
GTAAGAACCTTGAGTTACGGGTATCGTGTCTGT	1872
TTACTAATATCTCCAGCACCAAGCAAGTGCCTGGCA	1908
CGTAGTCCGTGCCCAAACATTGCAGAGAGGAGCT	1944
CATCAGCTCTGTCAGTGTTCAGTCTCATCTATT	1980
AAACAGGGTTGGTTTCTGGTTGCTAGGGAGACTT	2016
GTACTAACGCAACCTACTGTTCTAGATTCTTATCA	2052
CCGTGTTCATTTGACCACGTATCACCTTGTAT	2088
CAAGAGAAATGTGTGAAGCTTGTCTTATGCTGTAGC	2124
CATCTATATTGTAATTATCTCTATACAATTAAACA	2160
AATTTATTGACACCCTAAAAAAAAAAAAAAA	2196
AAAAAA	2202

Fig. 3 (A)

GCAGAGAGCAGGAAAAACAAGCTTGGTAAGCCTCC	36
GCCAGAGCAGAAAGAGCTGGGCGATTACGCCGGCT	72
TTCCCAGGCCGGTGTCCCGGTGTCCGGAGCCCCAA	108
GCCAGGAGCCTGTGGAACGGAAAATCGAGAGAGGCC	144
TGAACTGGGTCCCGGAGCACACCTTCGCCAGGGCG	180
CAGAGAAGGCTCACGCGACTAGTCCAACGCAGGGCC	216
TCGGCTCTCTGGAGCTGGCTGACCCTGGGGCGG	252
CAGATCACGATGCCCGCGCGCTCCCCGCCGCCTG	288
MetProAlaArgAlaProArgArgLeu	9
GTCCAGGGGCCTCGGGGACCTGGCTGCTGGGAAGC	324
ValGlnGlyProArgGlyThrTrpLeuLeuGlySer	21
CTCTGGGTCTGGGTGCTGTGCCGCCTGGGGATGGCG	360
LeuTrpValTrpValLeuCysGlyLeuGlyMetAla	33
GGCTCCCTGGGAACCCCACAGCCATGCCAGGCACCC	396
GlySerLeuGlyThrProGlnProCysGlnAlaPro	45
CAGCAGTGGGAGGGACGCCAGGTTCTGTACCAGCAG	432
GlnGlnTrpGluGlyArgGlnValLeuTyrGlnGln	57
AGCAGCGGGCACACAACCGCGCCCTGGTGTCTAC	468
SerSerGlyHisAsnAsnArgAlaLeuValSerTyr	69
GATGGTCTCAACCAGCGCGTGCAGGTGCTGGACGAG	504
AspGlyLeuAsnGlnArgValArgValLeuAspGlu	81
AGGAAAGCGCTGATCCCCTGCAAGAGATTATTTGAA	540
ArgLysAlaLeuIleProCysLysArgLeuPheGlu	93
TACATTTACTCTATAAGGAGGGAGTGATGTTTCAG	576
TyrIleLeuLeuTyrLysGluGlyValMetPheGln	105

Fig. 3 (B)

ATTGAACAAGCCACCAAACAGTGTGCAAAGATCCCC IleGluGlnAlaThrLysGlnCysAlaLysIlePro	612 117
TTGGTGGAATCCTGGGATCCTCTGGACATTCCCCAG LeuValGluSerTrpAspProLeuAspIleProGln	648 129
AATTCTACCTTGAAAGATCAGTACTCCATCGGAGGG AsnSerThrPheGluAspGlnTyrSerIleGlyGly	684 141
CCTCAGGAGCAGATCCTGGTCCAGGAGTGGTCTGAC ProGlnGluGlnIleLeuValGlnGluTrpSerAsp	720 153
AGAAGAACAGCAAGATCCTATGAAACTTGGATCGGC ArgArgThrAlaArgSerTyrGluThrTrpIleGly	756 165
GTTTATACAGCCAAGGATTGTTATCCGGTCCAGGAG ValTyrThrAlaLysAspCysTyrProValGlnGlu	792 177
ACCTTCATCAGGAACTACACTGTGGTCATGTCCACG ThrPheIleArgAsnTyrThrValValMetSerThr	828 189
CGGTTCTTGATGTGCAGCTAGGCATTAAGGACCCC ArgPhePheAspValGlnLeuGlyIleLysAspPro	864 201
TCTGTGTTCACCCCCACCAAGCACATGCCAGGCAGCG SerValPheThrProProSerThrCysGlnAlaAla	900 213
CAGCCAGAGAAGATGAGTGACGGCTGCTCCTGTGA GlnProGluLysMetSerAspGlyCysSerLeu***	936 224
ACTCGCCGAAC TGAAACCCAACCTCAGCTCTTAGTGA CCTTGTATGGCAATGGATTAGAGACTAGTTGAAAG	972 1008
TAACTCTTCACTGAAAATAAGCTAATTAGGAAG	1044
ATAAACCCATGTGGGCTTGCTGTACATCTGACTG	1080
TGGCTGCTCAGCTCTGTTGAGAAGGAAAGGGGCC	1116
ATCCTTCTGTGAGCAGGTGGTAGTCAGTGCCATA	1152

Fig. 3 (C)

GAGTAGGAAAGGGCGGGGTGGGGTCAGCACAGGA	1188
TTTGCCTCTGCAGGGTGAGACTTTATTATTGCCA	1224
ATAAGAACATCGAAGGTGATAATAAGATATAGAATGCT	1260
TTTGTTCAGTTCTCCCTTACAAAGAAAGTCCCTG	1296
CTTGTCTGCACCAGGAAGCAAGAGCTCCCAGTGAC	1332
ACCACCCCTGCCTCTGGTTACTATAAGATGAGCCT	1368
TTAAGATTCTTCTAGACTAAATTGTGCCATGG	1404
CCCACTGGATGTAGATATTCTACAAGGAAGTAGAAA	1440
CTTTTAATACGAAGTAATGATTCCCTCTAAAGGGAAA	1476
GGAAGTTTAAGAGGGAGGCTGGACAATCTTAGTA	1512
TTTACACGTGAGATGAAATGAAGAGTCCCGTGTGCT	1548
GCTCTGTGTGCAAGAGTACTGACCGCTCTGCTGAAC	1584
CTTCATGTCTTTCTAGTGGCAACCAGGCTTCAA	1620
AATAGCACTGACCTGGGAGGCCCAAGTAAGGCCA	1656
AGAAAGTCTCTGCTACTCTAATCTTTACGTATTAAA	1692
TGCACTAGGCTAGTAGCCCTGCCTTCCTTCCTG	1728
AAACTCTTCAACACAACGTGTCTATATGACTACG	1764
GCTCATGCTTCCAAGGTCAAGTCACATGTGACCTCT	1800
GTGAGCTGTTCCCTGCCTGAATTATTGCATCTTA	1836
CACCTTGGCATGCCTGCTACAATACTCATTATGC	1872
TGTGTGGGATTCCTGATTACTAGAAGCTGACCTCT	1908
GCTATCCTGGTAAGAACGCCCTGAGTACGGTACC	1944
ATGCTCTGTTACTTAGGATCTCCAGCACCAAGCA	1980
AGTGCCTGGCACATAGTCTGTGCCCTAACATTGT	2016
AGAAAGGAGCTCACCAAGCTCTGTCACTGTTAGTT	2052
CTTCATCTATTAAACAGGGTGGTTTCTGGTGC	2088
TAGGGAGACTTATAGTAATACAACCTACTATTCTAG	2124
ATTCTTCTTATCGCTGTGTTTATTGCCATGTATC	2160
ATCTTTGTTATCAAGAGAAGTGTATGATGCTTGCT	2196
TTATGCCATAGCCATCTATATTGTAATTATCTATA	2232
CAATTAAACAAATTAAATGAACCCCTATGAATTATTC	2268
TTTGATGTGTTGTTGTAAAGAAATATGGAGGAA	2304
CTGAATTATAAAGAAAATAAATCCTCTGTAATAA	2340

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Fig. 3 (D)

TCAAATAAAGTACTTCCCATAATCAAAACCAAAAAA 2376
AAAAAAAAAAAAAAAAAAAAAAA 2403

Fig. 4

Fig. 5

Fig. 6

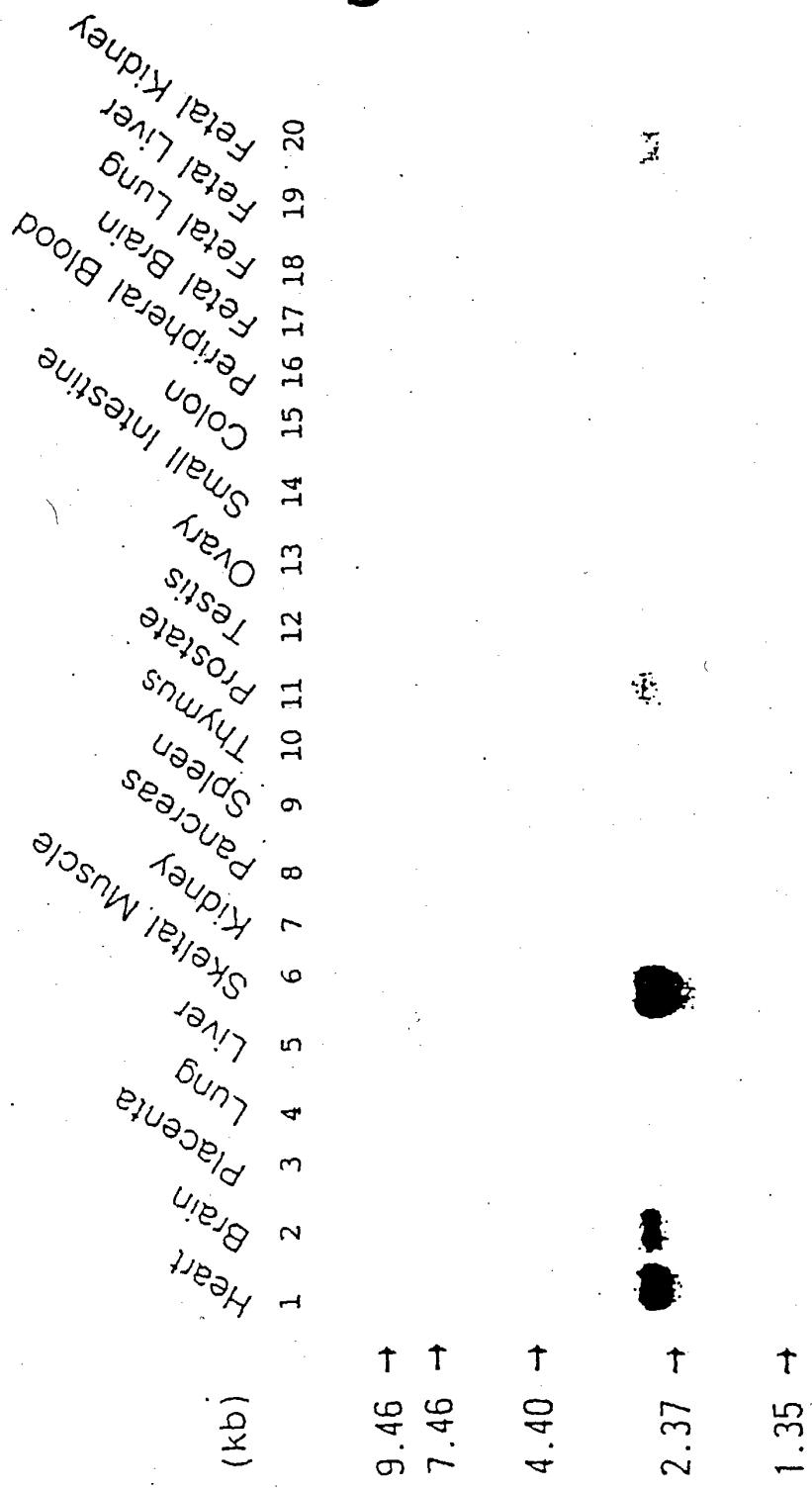


Fig. 7

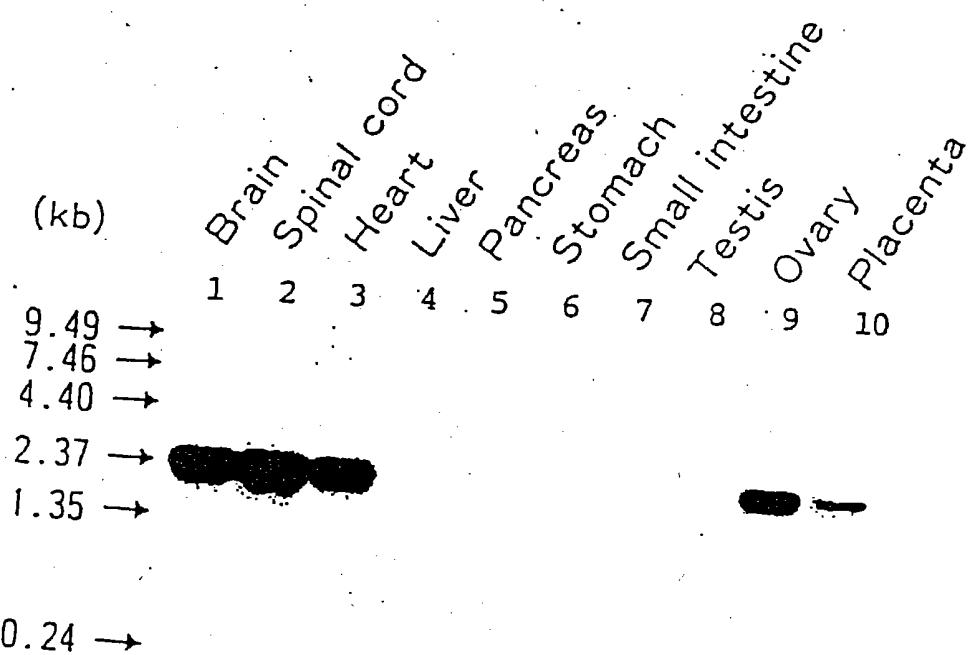


Fig. 8

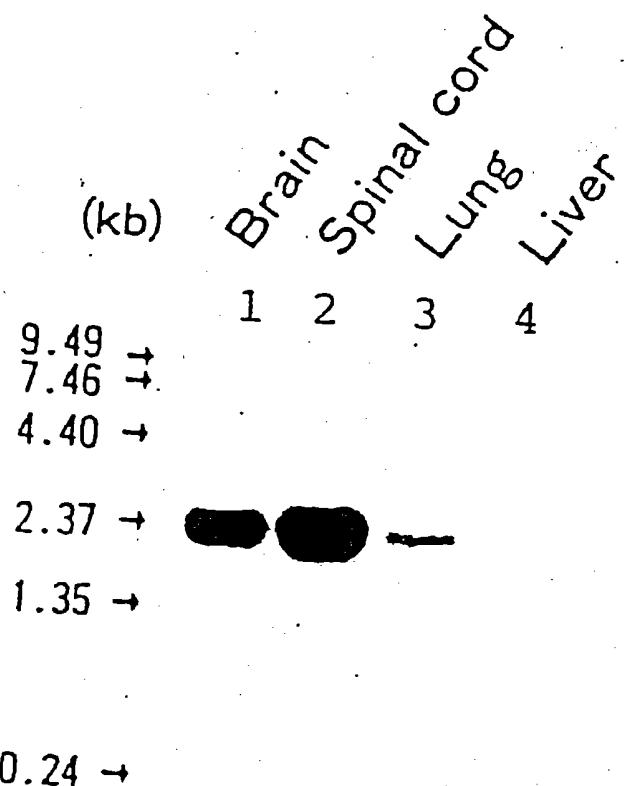


Fig. 9

